

SEQUENCE LISTING

<110> Oppermann, Hermann
 Tai, Mei-Sheng
 McCartney, John

<120> Modified TGF-beta Superfamily Proteins

<130> STK-075

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<170> PatentIn Ver. 2.0

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<212> PRT

<213> Drosophila melanogaster

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Gly	Cys	His
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Gly	Cys	Arg
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Cys Gly Cys Arg
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Gly Cys Ser
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<213> Bos taurus

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Gly Cys Arg
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<213> Gallus gallus

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Gly Cys Arg
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<213> *Mus musculus*

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Gly Cys Arg
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Gly Cys Gly
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<213> Homo sapiens

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Gly Cys Ser
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Gly Cys His
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<212> PRT
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Gly Cys His
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<210> 28
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Gly Cys His
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<220>
<223> TGF-Betal

<400> 29
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Cys Ser

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<212> PRT
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Cys Ser

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<223> TGF-Beta3

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Cys Ser

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<213> Gallus gallus

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<223> TGF-Beta4

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Cys Ser

<210> 33
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<212> PRT
<213> *Xenopus laevis*

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<223> TGF-Beta5

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<213> *Strongylocentrotus purpuratus*

<220>
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Gly Cys Arg
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<213> *Xenopus laevis*

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<210> 36
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21

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Arg Ser Leu Arg Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
5 10 15

ccc ctg ttc ctg ctg cgc tcc gcc ctg gcc gac ttc agc ctg gac aac 153
Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
20 25 30 35

gag gtg cac tcg agc ttc atc cac cgg cgc ctc cgc agc cag gag cgg 201
Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
40 45 50

cgg gag atg cag cgc gag atc ctc tcc att ttg ggc ttg ccc cac cgc 249
Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
55 60 65

ccg cgc ccg cac ctc cag ggc aag cac aac tcg gca ccc atg ttc atg	297
Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met	
70 75 80	
ctg gac ctg tac aac gcc atg gcg gtg gag gag ggc ggc ggg ccc ggc	345
Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly	
85 90 95	
ggc cag ggc ttc tcc tac ccc tac aag gcc gtc ttc agt acc cag ggc	393
Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly	
100 105 110 115	
ccc cct ctg gcc agc ctg caa gat agc cat ttc ctc acc gac gcc gac	441
Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp	
120 125 130	
atg gtc atg agc ttc gtc aac ctc gtg gaa cat gac aag gaa ttc ttc	489
Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe	
135 140 145	
cac cca cgc tac cac cat cga gag ttc cgg ttt gat ctt tcc aag atc	537
His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile	
150 155 160	
cca gaa ggg gaa gct gtc acg gca gcc gaa ttc cgg atc tac aag gac	585
Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp	
165 170 175	
tac atc cgg gaa cgc ttc gac aat gag acg ttc cgg atc agc gtt tat	633
Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr	
180 185 190 195	
cag gtg ctc cag gag cac ttg ggc agg gaa tcg gat ctc ttc ctg ctc	681
Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu	
200 205 210	
gac agc cgt acc ctc tgg gcc tcg gag gag ggc tgg ctg gtg ttt gac	729
Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp	
215 220 225	
atc aca gcc acc agc aac cac ttg gtg gtc aat ccg cgg cac aac ctg	777
Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu	
230 235 240	
ggc ctg cag ctc tcg gtg gag acg ctg gat ggg cag agc atc aac ccc	825
Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro	
245 250 255	
aag ttg gcg ggc ctg att ggg cgg cac ggg ccc cag aac aag cag ccc	873
Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro	
260 265 270 275	
ttc atg gtg gct ttc ttc aag gcc acg gag gtc cac ttc cgc agc atc	921
Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile	
280 285 290	

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 Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro
 295 300 305

aag aac cag gaa gcc ctg cgg atg gcc aac gtg gca gag aac agc agc 1017
 Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser
 310 315 320

agc gac cag agg cag gcc tgt aag aag cac gag ctg tat gtc agc ttc 1065
 Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe
 325 330 335

cga gac ctg ggc tgg cag gac tgg atc atc gcg cct gaa ggc tac gcc 1113
 Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala
 340 345 350 355

gcc tac tac tgt gag ggg gag tgt gcc ttc cct ctg aac tcc tac atg 1161
 Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met
 360 365 370

aac gcc acc aac cac gcc atc gtg cag acg ctg gtc cac ttc atc aac 1209
 Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn
 375 380 385

ccg gaa acg gtg ccc aag ccc tgc tgt gcg ccc acg cag ctc aat gcc 1257
 Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala
 390 395 400

atc tcc gtc ctc tac ttc gat gac agc tcc aac gtc atc ctg aag aaa 1305
 Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys
 405 410 415

tac aga aac atg gtg gtc cgg gcc tgt ggc tgc cac tagctcctcc 1351
 Tyr Arg Asn Met Val Arg Ala Cys Gly Cys His
 420 425 430

gagaattcag accctttggg gccaaagtttt tctggatcct ccattgctcg ccttggccag 1411
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 ggcgtggcaa ggggtgggca cattggtgtc tgtgcgaaag gaaaattgac ccggaagtgc 1771
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<210> 39
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 <212> PRT
 <213> Homo sapiens

<400> 39

Met	His	Val	Arg	Ser	Leu	Arg	Ala	Ala	Ala	Pro	His	Ser	Phe	Val	Ala	
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Leu	Trp	Ala	Pro	Leu	Phe	Leu	Leu	Arg	Ser	Ala	Leu	Ala	Asp	Phe	Ser	
			20					25					30			
Leu	Asp	Asn	Glu	Val	His	Ser	Ser	Phe	Ile	His	Arg	Arg	Leu	Arg	Ser	
	35						40					45				
Gln	Glu	Arg	Arg	Glu	Met	Gln	Arg	Glu	Ile	Leu	Ser	Ile	Leu	Gly	Leu	
	50					55					60					
Pro	His	Arg	Pro	Arg	Pro	His	Leu	Gln	Gly	Lys	His	Asn	Ser	Ala	Pro	
65					70					75					80	
Met	Phe	Met	Leu	Asp	Leu	Tyr	Asn	Ala	Met	Ala	Val	Glu	Glu	Gly	Gly	
				85					90					95		
Gly	Pro	Gly	Gly	Gln	Gly	Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser	
			100					105						110		
Thr	Gln	Gly	Pro	Pro	Leu	Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	
			115					120					125			
Asp	Ala	Asp	Met	Val	Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	
	130					135					140					
Glu	Phe	Phe	His	Pro	Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	
145					150					155					160	
Ser	Lys	Ile	Pro	Glu	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	
				165					170						175	
Tyr	Lys	Asp	Tyr	Ile	Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Arg	Ile	
			180					185						190		
Ser	Val	Tyr	Gln	Val	Leu	Gln	Glu	His	Leu	Gly	Arg	Glu	Ser	Asp	Leu	
			195				200					205				
Phe	Leu	Leu	Asp	Ser	Arg	Thr	Leu	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	
	210					215					220					
Val	Phe	Asp	Ile	Thr	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	
225					230					235					240	
His	Asn	Leu	Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	
			245						250					255		
Ile	Asn	Pro	Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	
			260					265					270			
Lys	Gln	Pro	Phe	Met	Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Phe	
		275					280					285				
Arg	Ser	Ile	Arg	Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	

290		295		300
Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu				
305		310		315 320
Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr				
	325		330	335
Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu				
	340		345	350
Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn				
	355		360	365
Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His				
	370		375	380
Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln				
	385		390 395	400
Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile				
	405		410	415
Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His				
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<210> 40
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 <213> Homo sapiens

<220>
 <223> TGF-Betal

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 Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp
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 Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly
 20 25 30
 Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu
 35 40 45
 Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys
 50 55 60
 Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg
 65 70 75 80
 Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys
 85 90 95
 Cys Ser

<210> 41
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 <212> PRT
 <213> Homo sapiens

<220>
 <223> TGF-Beta2

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 20 25 30
 Ala Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu
 35 40 45
 Ser Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys
 50 55 60
 Val Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys
 65 70 75 80
 Thr Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys
 85 90 95
 Cys Ser

<210> 42
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<220>
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 20 25 30
 Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu
 35 40 45
 Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys
 50 55 60
 Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg
 65 70 75 80
 Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys

85

90

95

Cys Ser

<210> 43

<211> 98

<212> PRT

<213> Gallus gallus

<220>

<223> TGF-Beta4

<400> 43

Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gln Trp
 1 5 10 15

Lys Trp Ile His Glu Pro Lys Gly Tyr Met Ala Asn Phe Cys Met Gly
 20 25 30

Pro Cys Pro Tyr Ile Trp Ser Ala Asp Thr Gln Tyr Thr Lys Val Leu
 35 40 45

Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys
 50 55 60

Val Pro Gln Thr Leu Asp Pro Leu Pro Ile Ile Tyr Tyr Val Gly Arg
 65 70 75 80

Asn Val Arg Val Glu Gln Leu Ser Asn Met Val Val Arg Ala Cys Lys
 85 90 95

Cys Ser

<210> 44

<211> 98

<212> PRT

<213> Xenopus laevis

<220>

<223> TGF-Beta5

<400> 44

Cys Cys Val Lys Pro Leu Tyr Ile Asn Phe Arg Lys Asp Leu Gly Trp
 1 5 10 15

Lys Trp Ile His Glu Pro Lys Gly Tyr Glu Ala Asn Tyr Cys Leu Gly
 20 25 30

Asn Cys Pro Tyr Ile Trp Ser Met Asp Thr Gln Tyr Ser Lys Val Leu
 35 40 45

Ser Leu Tyr Asn Gln Asn Asn Pro Gly Ala Ser Ile Ser Pro Cys Cys
 50 55 60

Val Pro Asp Val Leu Glu Pro Leu Pro Ile Ile Tyr Tyr Val Gly Arg
65 70 75 80

Thr Ala Lys Val Glu Gln Leu Ser Asn Met Val Val Arg Ser Cys Asn
85 90 95

Cys Ser

<210> 45
<211> 102
<212> PRT
<213> *Drosophila melanogaster*

<220>
<223> DPP

<400> 45
Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asp
1 5 10 15

Asp Trp Ile Val Ala Pro Leu Gly Tyr Asp Ala Tyr Tyr Cys His Gly
20 25 30

Lys Cys Pro Phe Pro Leu Ala Asp His Phe Asn Ser Thr Asn His Ala
35 40 45

Val Val Gln Thr Leu Val Asn Asn Met Asn Pro Gly Lys Val Pro Lys
50 55 60

Ala Cys Cys Val Pro Thr Gln Leu Asp Ser Val Ala Met Leu Tyr Leu
65 70 75 80

Asn Asp Gln Ser Thr Val Val Leu Lys Asn Tyr Gln Glu Met Thr Val
85 90 95

Val Gly Cys Gly Cys Arg
100

<210> 46
<211> 102
<212> PRT
<213> *Xenopus laevis*

<220>
<223> VG1

<400> 46
Cys Lys Lys Arg His Leu Tyr Val Glu Phe Lys Asp Val Gly Trp Gln
1 5 10 15

Asn Trp Val Ile Ala Pro Gln Gly Tyr Met Ala Asn Tyr Cys Tyr Gly
20 25 30

Glu Cys Pro Tyr Pro Leu Thr Glu Ile Leu Asn Gly Ser Asn His Ala
 35 40 45
 Ile Leu Gln Thr Leu Val His Ser Ile Glu Pro Glu Asp Ile Pro Leu
 50 55 60
 Pro Cys Cys Val Pro Thr Lys Met Ser Pro Ile Ser Met Leu Phe Tyr
 65 70 75 80
 Asp Asn Asn Asp Asn Val Val Leu Arg His Tyr Glu Asn Met Ala Val
 85 90 95
 Asp Glu Cys Gly Cys Arg
 100

<210> 47
 <211> 102
 <212> PRT
 <213> Mus musculus

<220>
 <223> VGR1

<400> 47
 Cys Lys Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln
 1 5 10 15
 Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly
 20 25 30
 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95
 Arg Ala Cys Gly Cys His
 100

<210> 48
 <211> 118
 <212> PRT
 <213> Drosophila melanogaster

<220>
 <223> 60A

<400> 48
 Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp His

1	5	10	15
Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser Gly	20	25	30
Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala	35	40	45
Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro Lys	50	55	60
Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr His	65	70	75
Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr His	85	90	95
Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile Val	100	105	110
Lys Ser Cys Gly Cys His	115		

<210> 49
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <223> BMP-2A

<400> 49
Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
1 5 10 15
Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly
20 25 30
Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala
35 40 45
Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala
50 55 60
Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp
65 70 75 80
Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu
85 90 95
Gly Cys Gly Cys Arg
100

<210> 50
 <211> 103

<212> PRT
<213> Homo sapiens

<220>
<223> BMP3

<400> 50
Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Ser
1 5 10 15
Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ser Gly
20 25 30
Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His Ala
35 40 45
Thr Ile Gln Ser Ile Val Arg Ala Val Gly Val Val Pro Gly Ile Pro
50 55 60
Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu Phe
65 70 75 80
Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met Thr
85 90 95
Val Glu Ser Cys Ala Cys Arg
100

<210> 51
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<223> BMP-4

<400> 51
Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
1 5 10 15
Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly
20 25 30
Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala
35 40 45
Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala
50 55 60
Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp
65 70 75 80
Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu
85 90 95
Gly Cys Gly Cys Arg

100

<210> 52
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<223> BMP-5

<400> 52
Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
1 5 10 15
Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly
20 25 30
Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
35 40 45
Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys
50 55 60
Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
65 70 75 80
Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
85 90 95
Arg Ser Cys Gly Cys His
100

<210> 53
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<223> BMP-6

<400> 53
Cys Arg Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln
1 5 10 15
Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly
20 25 30
Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
35 40 45
Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro Lys
50 55 60
Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
65 70 75 80

Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
85 90 95

Arg Ala Cys Gly Cys His
100

<210> 54
<211> 103
<212> PRT
<213> Gallus gallus

<220>
<223> DORSALIN

<400> 54
Cys Arg Arg Thr Ser Leu His Val Asn Phe Lys Glu Ile Gly Trp Asp
1 5 10 15

Ser Trp Ile Ile Ala Pro Lys Asp Tyr Glu Ala Phe Glu Cys Lys Gly
20 25 30

Gly Cys Phe Phe Pro Leu Thr Asp Asn Val Thr Pro Thr Lys His Ala
35 40 45

Ile Val Gln Thr Leu Val His Leu Gln Asn Pro Lys Lys Ala Ser Lys
50 55 60

Ala Cys Cys Val Pro Thr Lys Leu Asp Ala Ile Ser Ile Leu Tyr Lys
65 70 75 80

Asp Asp Ala Gly Val Pro Thr Leu Ile Tyr Asn Tyr Glu Gly Met Lys
85 90 95

Val Ala Glu Cys Gly Cys Arg
100

<210> 55
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<223> OP-1

<400> 55
Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
1 5 10 15

Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly
20 25 30

Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala Thr Asn His Ala
35 40 45

Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Glu Thr Val Pro Lys
50 55 60

Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val Leu Tyr Phe
65 70 75 80

Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
85 90 95

Arg Ala Cys Gly Cys His
100

<210> 56
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<223> OP-2

<400> 56
Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu
1 5 10 15

Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly
20 25 30

Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala
35 40 45

Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys
50 55 60

Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr
65 70 75 80

Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val
85 90 95

Lys Ala Cys Gly Cys His
100

<210> 57
<211> 102
<212> PRT
<213> Mus musculus

<220>
<223> OP-3

<400> 57
Cys Arg Arg His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Leu
1 5 10 15

Asp Ser Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Ala Gly

20 25 30
 Glu Cys Ile Tyr Pro Leu Asn Ser Cys Met Asn Ser Thr Asn His Ala
 35 40 45
 Thr Met Gln Ala Leu Val His Leu Met Lys Pro Asp Ile Ile Pro Lys
 50 55 60
 Val Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Leu Leu Tyr Tyr
 65 70 75 80
 Asp Arg Asn Asn Asn Val Ile Leu Arg Arg Glu Arg Asn Met Val Val
 85 90 95
 Gln Ala Cys Gly Cys His
 100

<210> 58
 <211> 107
 <212> PRT
 <213> Mus musculus

<220>
 <223> GDF-1

<400> 58
 Cys Arg Thr Arg Arg Leu His Val Ser Phe Arg Glu Val Gly Trp His
 1 5 10 15
 Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn Phe Cys Gln Gly
 20 25 30
 Thr Cys Ala Leu Pro Glu Thr Leu Arg Gly Pro Gly Gly Pro Pro Ala
 35 40 45
 Leu Asn His Ala Val Leu Arg Ala Leu Met His Ala Ala Ala Pro Thr
 50 55 60
 Pro Gly Ala Gly Ser Pro Cys Cys Val Pro Glu Arg Leu Ser Pro Ile
 65 70 75 80
 Ser Val Leu Phe Phe Asp Asn Ser Asp Asn Val Val Leu Arg His Tyr
 85 90 95
 Glu Asp Met Val Val Asp Glu Cys Gly Cys Arg
 100 105

<210> 59
 <211> 101
 <212> PRT
 <213> Mus musculus

<220>
 <223> GDF-3

<400> 59

Cys His Arg His Gln Leu Phe Ile Asn Phe Gln Asp Leu Gly Trp His
1 5 10 15

Lys Trp Val Ile Ala Pro Lys Gly Phe Met Ala Asn Tyr Cys His Gly
20 25 30

Glu Cys Pro Phe Ser Met Thr Thr Tyr Leu Asn Ser Ser Asn Tyr Ala
35 40 45

Phe Met Gln Ala Leu Met His Met Ala Asp Pro Lys Val Pro Lys Ala
50 55 60

Val Cys Val Pro Thr Lys Leu Ser Pro Ile Ser Met Leu Tyr Gln Asp
65 70 75 80

Ser Asp Lys Asn Val Ile Leu Arg His Tyr Glu Asp Met Val Val Asp
85 90 95

Glu Cys Gly Cys Gly
100

<210> 60

<211> 102

<212> PRT

<213> Mus musculus

<220>

<223> GDF-9

<400> 60

Cys Glu Leu His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp
1 5 10 15

Asn Trp Ile Val Ala Pro His Arg Tyr Asn Pro Arg Tyr Cys Lys Gly
20 25 30

Asp Cys Pro Arg Ala Val Arg His Arg Tyr Gly Ser Pro Val His Thr
35 40 45

Met Val Gln Asn Ile Ile Tyr Glu Lys Leu Asp Pro Ser Val Pro Arg
50 55 60

Pro Ser Cys Val Pro Gly Lys Tyr Ser Pro Leu Ser Val Leu Thr Ile
65 70 75 80

Glu Pro Asp Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Ile Ala
85 90 95

Thr Arg Cys Thr Cys Arg
100

<210> 61

<211> 105

<212> PRT

<213> Homo sapiens

<220>

<223> INHIBIN-Alpha

<400> 61

Cys His Arg Val Ala Leu Asn Ile Ser Phe Gln Glu Leu Gly Trp Glu
1 5 10 15

Arg Trp Ile Val Tyr Pro Pro Ser Phe Ile Phe His Tyr Cys His Gly
20 25 30

Gly Cys Gly Leu His Ile Pro Pro Asn Leu Ser Leu Pro Val Pro Gly
35 40 45

Ala Pro Pro Thr Pro Ala Gln Pro Tyr Ser Leu Leu Pro Gly Ala Gln
50 55 60

Pro Cys Cys Ala Ala Leu Pro Gly Thr Met Arg Pro Leu His Val Arg
65 70 75 80

Thr Thr Ser Asp Gly Gly Tyr Ser Phe Lys Tyr Glu Thr Val Pro Asn
85 90 95

Leu Leu Thr Gln His Cys Ala Cys Ile
100 105

<210> 62

<211> 106

<212> PRT

<213> Bos taurus

<220>

<223> INHIBIN-BetaA

<400> 62

Cys Cys Lys Lys Gln Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn
1 5 10 15

Asp Trp Ile Ile Ala Pro Ser Gly Tyr His Ala Asn Tyr Cys Glu Gly
20 25 30

Glu Cys Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe
35 40 45

His Ser Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe
50 55 60

Ala Asn Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser
65 70 75 80

Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln
85 90 95

Asn Met Ile Val Glu Glu Cys Gly Cys Ser
100 105

<210> 63
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <223> INHIBIN-BetaB

<400> 63
 Cys Cys Lys Lys Gln Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn
 1 5 10 15
 Asp Trp Ile Ile Ala Pro Ser Gly Tyr His Ala Asn Tyr Cys Glu Gly
 20 25 30
 Glu Cys Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe
 35 40 45
 His Ser Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe
 50 55 60
 Ala Asn Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser
 65 70 75 80
 Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln
 85 90 95
 Asn Met Ile Val Glu Glu Cys Gly Cys Ser
 100 105

<210> 64
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: TGF-B
 SUBGROUP SEQUENCE PATTERN

<220>
 <223> Each Xaa is independently selected from a group of
 one or more specified amino acids as defined in
 the specification

<400> 64
 Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg Xaa Asp Leu Gly Trp
 1 5 10 15
 Lys Trp Ile His Glu Pro Lys Gly Tyr Xaa Ala Asn Phe Cys Xaa Gly
 20 25 30
 Xaa Cys Pro Tyr Xaa Trp Ser Xaa Asp Thr Gln Xaa Ser Xaa Val Leu
 35 40 45

Xaa Leu Tyr Asn Xaa Xaa Asn Pro Xaa Ala Ser Ala Xaa Pro Cys Cys
 50 55 60
 Val Pro Gln Xaa Leu Glu Pro Leu Xaa Ile Xaa Tyr Tyr Val Gly Arg
 65 70 75 80
 Xaa Xaa Lys Val Glu Gln Leu Ser Asn Met Xaa Val Xaa Ser Cys Lys
 85 90 95
 Cys Ser

<210> 65
 <211> 104
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Each Xaa is independently selected from a group of
 one or more specified amino acids as defined in
 the specification

<220>
 <223> Description of Artificial Sequence: VG/DPP
 SUBGROUP SEQUENCE PATTERN

<400> 65
 Cys Xaa Xaa Xaa Xaa Leu Tyr Val Xaa Phe Xaa Asp Xaa Gly Trp Xaa
 1 5 10 15
 Asp Trp Ile Ile Ala Pro Xaa Gly Tyr Xaa Ala Xaa Tyr Cys Xaa Gly
 20 25 30
 Xaa Cys Xaa Phe Pro Leu Xaa Xaa Xaa Xaa Asn Xaa Thr Asn His Ala
 35 40 45
 Ile Xaa Gln Thr Leu Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro
 50 55 60
 Lys Xaa Cys Cys Xaa Pro Thr Xaa Leu Xaa Ala Xaa Ser Xaa Leu Tyr
 65 70 75 80
 Xaa Asp Xaa Xaa Xaa Xaa Xaa Val Xaa Leu Xaa Xaa Tyr Xaa Xaa Met
 85 90 95
 Xaa Val Xaa Xaa Cys Gly Cys Xaa
 100

<210> 66
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: GDF SUBGROUP

PATTERN

<220>

<223> Each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification

<400> 66

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Trp Xaa
1 5 10 15

Xaa Trp Xaa Xaa Ala Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Gly
20 25 30

Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Pro Xaa Xaa Xaa Xaa Xaa Xaa Cys Val Pro Xaa Xaa Xaa Ser Pro Xaa
65 70 75 80

Ser Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr
85 90 95

Glu Asp Met Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa
100 105

<210> 67

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: INHIBIN
SUBGROUP PATTERN

<220>

<223> Each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification

<400> 67

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa
1 5 10 15

Xaa Trp Ile Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Tyr Cys Xaa Gly
20 25 30

Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa
100 105

<210> 68
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<223> Mature H2223 mutant

<400> 68
Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys
1 5 10 15

Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser
20 25 30

Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
35 40 45

Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
50 55 60

Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
65 70 75 80

Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro
85 90 95

Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
100 105 110

Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
115 120 125

Glu Asp Met Val Val Glu Ala Cys Gly Cys Arg
130 135

<210> 69
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<223> Trypsin truncated H2223 mutant

<400> 69
Met Ala Asn Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys

1	5	10	15												
Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
		20						25					30		
Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu
		35					40					45			
Cys	Ala	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala	Thr	Asn	His	Ala	Ile
	50					55					60				
Val	Gln	Thr	Leu	Val	His	Phe	Ile	Asn	Pro	Glu	Thr	Val	Pro	Lys	Pro
	65				70					75					80
Cys	Cys	Ala	Pro	Thr	Gln	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe	Asp
				85				90						95	
Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Glu	Asp	Met	Val	Val	Glu
			100					105					110		
Ala	Cys	Gly	Cys	Arg											
		115													

<210> 70

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer #1

<220>

<221> CDS

<222> (1)..(33)

<400> 70

gcg ccc acg cag ctc agc gct atc tcc gtc ctc
Ala Pro Thr Gln Leu Ser Ala Ile Ser Val Leu
1 5 10

33

<210> 71

<211> 11

<212> PRT

<213> Artificial Sequence

<400> 71

Ala Pro Thr Gln Leu Ser Ala Ile Ser Val Leu
1 5 10

<210> 72

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer #2

<400> 72

ctatctgcag ccacaagctt cgaccaccat gtcttcgtat ttc

43

<210> 73

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:complement of
Primer #2

<220>

<221> CDS

<222> (2)..(43)

<400> 73

g aaa tac gaa gac atg gtg gtc gaa gct tgt ggc tgc aga tag

43

Lys Tyr Glu Asp Met Val Val Glu Ala Cys Gly Cys Arg

1

5

10

<210> 74

<211> 13

<212> PRT

<213> Artificial Sequence

<400> 74

Lys Tyr Glu Asp Met Val Val Glu Ala Cys Gly Cys Arg

1

5

10

<210> 75

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:the sequence
between the T7 promoter, at the XbaI site, and the
ATG codon

<400> 75

tctagaataa ttttgttttaa cctttaagaa ggagatatac gatg

44

<210> 76

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer #3

<400> 76
taatacgact cactatagg 19

<210> 77
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer #4

<400> 77
gctgagctgc gtgggcgc 18

<210> 78
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: complement of
Primer #4

<220>
<221> CDS
<222> (1)..(18)

<400> 78
gcg ccc acg cag ctc agc 18
Ala Pro Thr Gln Leu Ser
1 5

<210> 79
<211> 6
<212> PRT
<213> Artificial Sequence

<400> 79
Ala Pro Thr Gln Leu Ser
1 5

<210> 80
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer #5

<400> 80
ggatcctatc tgcagccaca agc 23

<210> 81
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: complement of
Primer #5

<220>
<221> CDS
<222> (1)..(18)

<400> 81
gct tgt ggc tgc aga tag gatcc
Ala Cys Gly Cys Arg
1 5

23

<210> 82
<211> 5
<212> PRT
<213> Artificial Sequence

<400> 82
Ala Cys Gly Cys Arg
1 5

<210> 83
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<223> CDMP-1/GDF-5

<400> 83
Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp Asp
1 5 10 15
Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu Gly
20 25 30
Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala
35 40 45
Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro Pro
50 55 60
Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe Ile
65 70 75 80
Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val
85 90 95

Glu Ser Cys Gly Cys Arg
100

<210> 84
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<223> CDMP-2/GDF-6

<400> 84
Cys Ser Lys Lys Pro Leu His Val Asn Phe Lys Glu Leu Gly Trp Asp
1 5 10 15
Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu Gly
20 25 30
Val Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala
35 40 45
Ile Ile Gln Thr Leu Met Asn Ser Met Asp Pro Gly Ser Thr Pro Pro
50 55 60
Ser Cys Cys Val Pro Thr Lys Leu Thr Pro Ile Ser Ile Leu Tyr Ile
65 70 75 80
Asp Ala Gly Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val
85 90 95
Glu Ser Cys Gly Cys Arg
100

<210> 85
<211> 102
<212> PRT
<213> Mus musculus

<220>
<223> GDF-6

<400> 85
Cys Ser Arg Lys Pro Leu His Val Asn Phe Lys Glu Leu Gly Trp Asp
1 5 10 15
Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu Gly
20 25 30
Val Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala
35 40 45
Ile Ile Gln Thr Leu Met Asn Ser Met Asp Pro Gly Ser Thr Pro Pro
50 55 60
Ser Cys Cys Val Pro Thr Lys Leu Thr Pro Ile Ser Ile Leu Tyr Ile

65 70 75 80
 Asp Ala Gly Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val
 85 90 95

Glu Ser Cys Gly Cys Arg
 100

<210> 86
 <211> 102
 <212> PRT
 <213> Bos taurus

<220>
 <223> CDMP-2

<400> 86
 Cys Ser Lys Lys Pro Leu His Val Asn Phe Lys Glu Leu Gly Trp Asp
 1 5 10 15

Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu Gly
 20 25 30

Val Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala
 35 40 45

Ile Ile Gln Thr Leu Met Asn Ser Met Asp Pro Gly Ser Thr Pro Pro
 50 55 60

Ser Cys Cys Val Pro Thr Lys Leu Thr Pro Ile Ser Ile Leu Tyr Ile
 65 70 75 80

Asp Ala Gly Asn Asn Val Val Tyr Asn Glu Tyr Glu Glu Met Val Val
 85 90 95

Glu Ser Cys Gly Cys Arg
 100

<210> 87
 <211> 102
 <212> PRT
 <213> Mus musculus

<220>
 <223> GDF-7

<400> 87
 Cys Ser Arg Lys Ser Leu His Val Asp Phe Lys Glu Leu Gly Trp Asp
 1 5 10 15

Asp Trp Ile Ile Ala Pro Leu Asp Tyr Glu Ala Tyr His Cys Glu Gly
 20 25 30

Val Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala
 35 40 45

Ile Ile Gln Thr Leu Leu Asn Ser Met Ala Pro Asp Ala Ala Pro Ala
50 55 60

Ser Cys Cys Val Pro Ala Arg Leu Ser Pro Ile Ser Ile Leu Tyr Ile
65 70 75 80

Asp Ala Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val
85 90 95

Glu Ala Cys Gly Cys Arg
100

<210> 88
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<223> CDMP-3 construct

<400> 88
Cys Ser Arg Lys Pro Leu His Val Asp Phe Lys Glu Leu Gly Trp Asp
1 5 10 15

Asp Trp Ile Ile Ala Pro Leu Asp Tyr Glu Ala Tyr His Cys Glu Gly
20 25 30

Leu Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala
35 40 45

Ile Ile Gln Thr Leu Leu Asn Ser Met Ala Pro Asp Ala Ala Pro Ala
50 55 60

Ser Cys Cys Val Pro Ala Arg Leu Ser Pro Ile Ser Ile Leu Tyr Ile
65 70 75 80

Asp Ala Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val
85 90 95

Glu Ala Cys Gly Cys Arg
100